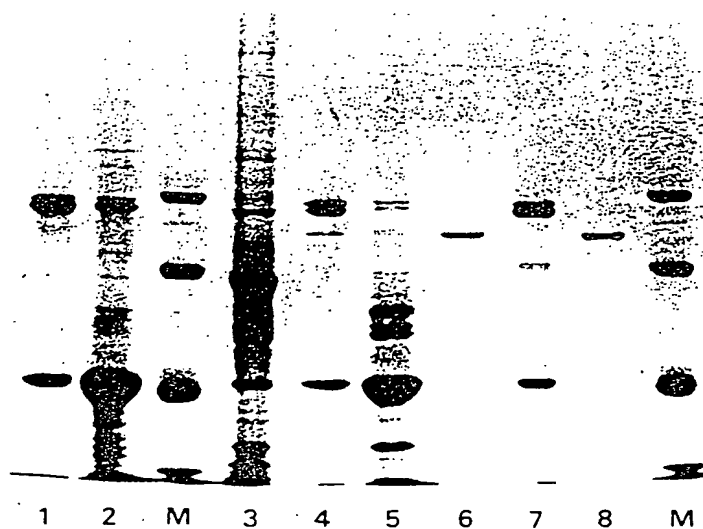




1/9

Fig. 1



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Fig. 2

adseverin C39	K V A H V K Q I P F D A
gelsolin	386 H I A N V E R V P F D A
villin	365 K V A K V E Q V K F D A

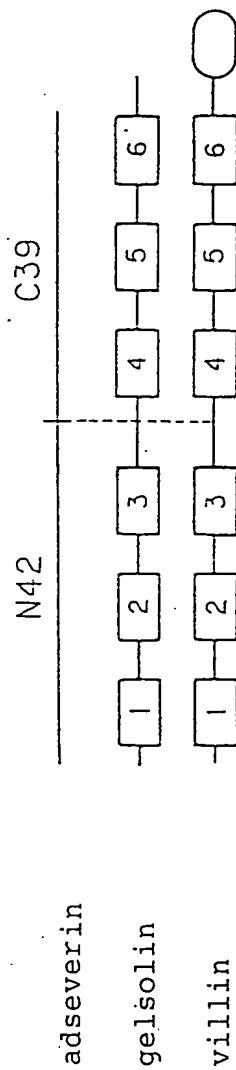


Fig. 3

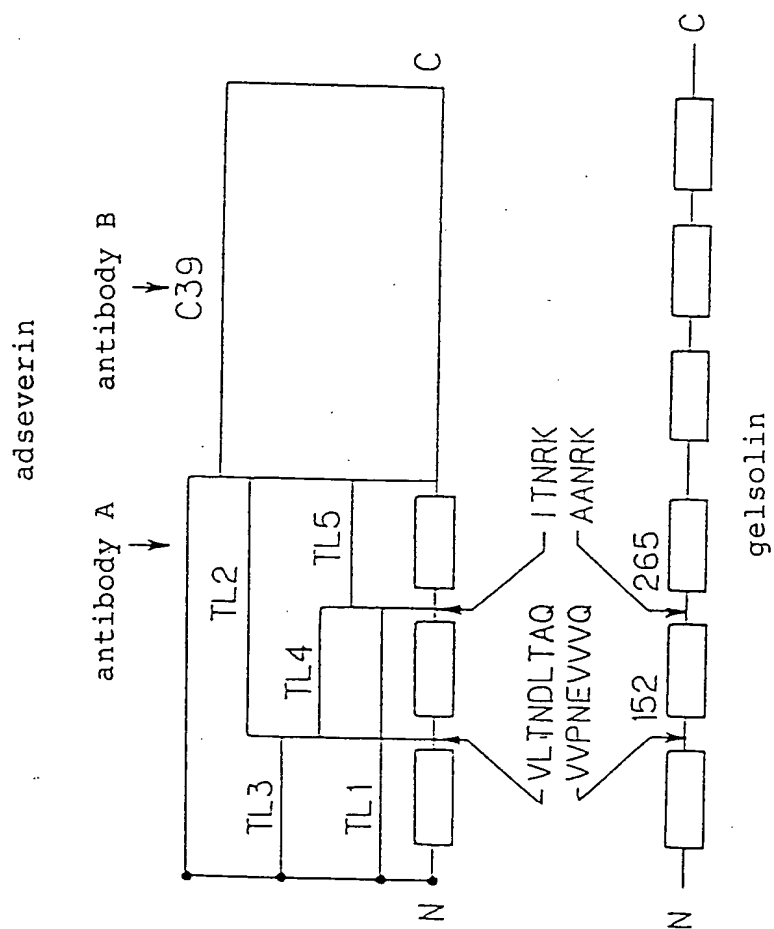
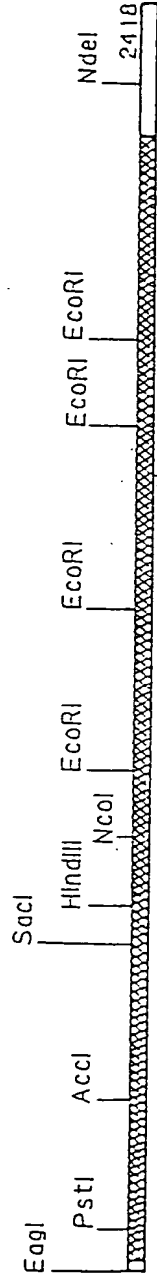


Fig. 4



PCR

19

5

21

Fig. 5A

ADS	008	EEFAR-AGK-R	AGLQVWRIE	KLELVPVPE	SAYGN	1
GEL	057	PEFLK-AGK-E	PGLQIWRIE	KEDLVPVPTN	LYGD	
VIL	007	QVKGS-LNITT	PGLQIWRIE	AMQMPVP	PSSTFGS	
ADS	385	AAQHHVDDGS	GKVQIWRIE	NNGRVEID	RNSYGE	4
GEL	434	AAQHGMDDDGT	GQKQIWRIE	GSNKVPVDP	PATYGG	
VIL	387	AAQQKMVDGGS	GEVQVWRIE	NLELVPVDS	KWLGH	
ADS	127	NHVLTNDLTAQ	RLHVKGR	-VVRATEV	PLSWDS	2
GEL	177	KHVVPNEVVQ	RLFQVKGR	-VVRATEV	PVSWES	
VIL	127	KHVEITNSYDVQ	RLHVKGR	NV-AGEV	EMSWKS	
ADS	503	GQAPAPPI--RL	FQVRRLAS	ITRIM-EV	DVDANS	5
GEL	556	GQTAPAST--RL	FQVRANSAG	ATRAV-EV	LPKAGA	
VIL	508	NLETGPST--RL	FQVQGTGAN	NTKAF-EV	PARANF	
ADS	245	NRKMAK-LYMV	SDASGSMKV	SLVAEENP	FSMAM	3
GEL	294	NRKLAK-LYKV	SNGAGTMSV	SLVADENP	FAQGA	
VIL	250	KAAL-K-LYHV	SDSEGNLVV	REVAI-RP	LITQDL	
ADS	610	ED-HPRLYGC	SNKTGRFII	EEVPGE--	FTQDD	6
GEL	662	MDAHPRLFAC	SNKIGRFVI	EEVPGE--	LMQED	
VIL	615	LVI-TPRLFEC	SNKTGRFLA	TEIP-D--	FNQDD	

Fig. 5B

ADS	F	YVG	D	A	YLV	LHTTQASRG---FTYR	L	HF	W	L	G	KECTQD	E	STA	A	1
GEL	F	FTG	D	A	YVI	LKTVQLRNGN--LQYD	L	HY	W	L	G	NECSQD	E	SGA	A	
VIL	F	FDG	D	C	YII	LAIH--KTASS-LSYD	I	HY	W	I	G	QDSSL	E	QGA	A	
ADS	F	YGG	D	C	YII	LYTYPR---GQI---	I	YT	W	Q	G	ANATRD	E	LTT	S	4
GEL	F	YGG	D	S	YII	LYNYRHGGRQGQI---	I	YN	W	Q	G	AQSTQD	E	VAA	S	
VIL	F	YGG	D	C	YLL	LYTYLIGEKQHYL---	L	YV	W	Q	G	SQASQD	E	ITA	S	
ADS	F	NKG	D	C	FII	-----DLGTE	I	YQ	W	C	G	SSCNKY	E	RLK	A	2
GEL	F	NNG	D	C	FIL	-----DLGNN	I	HQ	W	C	G	SNSNRY	E	RLK	A	
VIL	F	NRG	D	V	FLL	-----DLGKL	I	IQ	W	N	G	PESTRM	E	RLR	G	
ADS	L	NSN	D	V	FVL	-----KLRQNN	G	YI	W	I	G	KGSTQE	E	EKG	A	5
GEL	L	NSN	D	A	FVL	-----KT-PSA	A	YL	W	V	G	TGASEA	E	KTG	A	
VIL	L	NSN	D	V	FVL	-----KT-QSC	C	YL	W	C	G	KGCSGD	E	REM	A	
ADS	L	LSE	E	C	FIL	-----DHGAQKQ	I	FV	W	K	G	KDANPQ	E	RKA	A	3
GEL	L	KSE	D	C	FIL	-----DHGKDQK	I	FV	W	K	G	KQANTE	E	RKA	A	
VIL	L	SHE	D	C	YIL	-----DQG-GLK	I	YV	W	K	G	KKANEQ	E	KKG	A	
ADS	L	AED	D	V	MLL	-----DAWEQ	I	FI	W	I	G	KDANEV	E	KSE	S	6
GEL	L	ATD	D	V	MLL	-----DTWDQ	V	FV	W	V	G	KDSQEE	E	KTE	A	
VIL	L	EED	D	V	FLL	-----DVWDQ	V	FF	W	I	G	KHANEV	E	KKA	A	

← Motif B →

← Motif A →

Fig. 5C

ADS	AIETVQMDDYLGCKPVQNREL----	QG	Y	ES	TD	FV	G	YF	1
GEL	AIFTVQLDYLNGRAVQHREV-----	QG	F	ES	AT	FL	G	YF	
VIL	AIYTTQMDDFLKGRAVQHREV-----	QG	N	ES	EA	FR	G	YF	
ADS	AFLTVOIDRSLGGQAVQIRVS-----	QG	K	EP	AH	LL	S	LF	4
GEL	AILTAQLDDELGGTPVQSRVV-----	QG	K	EP	AH	LM	S	LF	
VIL	AYQAVIILDQKYNGEPPVQIRVP-----	MG	K	EP	PH	LM	S	IF	
ADS	SQVAIGIRDNERKGRAQLIVE-----	EG	S	EP	SE	LT	K	VL	2
GEL	TQVSKGIRDNERSGRARVHVSE-----	EG	T	EP	EA	ML	Q	VL	
VIL	MTLAKEIRDQERGGRTYVGVDGEN	EL	A	SP	-K	LM	E	VM	
ADS	EYVASVL-----KCKTSTIQ-----	EG	K	EP	EE	FW	N	SL	5
GEL	QELLRVL-----RAQPVQVA-----	EG	S	EP	DG	FW	E	AL	
VIL	KMVADTISRTEK-----QV-VV-----	EG	Q	EP	AN	FW	M	AL	
ADS	MKTAEFFLQOMNYSTNT-QIQVLP-	EG	G	ET	P	IF	KQ	FF	3
GEL	LKTASDFITKMDYPKQT-QVSVLP-	EG	G	ET	P	LF	KQ	FF	
VIL	MSHALNFIKAKQYPPST-QVEVQN-	DG	A	ES	A	VF	QQ	LF	
ADS	LKSAKIYLETDPGGRDKRTPIVIILK	QG	H	EP	PT	FT	GW	FL	6
GEL	LTSAKRYIETDPANRDRRTPITVVK	QG	F	EP	PS	FV	GW	FL	
VIL	ATTAQOEYLKTHPSGRDPETPIIVVK	QG	H	EP	PT	FT	GW	FL	


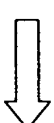
 Motif C 

Fig. 5D

ADS	-	KGGLKY---KA	GGVASGL	126	
GEL	-	KSGLKY---KK	GGVASGF	176	
VIL	-	KQGLVI---RK	GGVASGM	126	1
ADS	-	---KDKPLIY	KNGTSKKE	502	
GEL	-	---GGKPMIY	KGGSREG	555	
VIL	-	---KGR-MVY	QGGTSRTN	507	4
ADS	-	---GEKPKLRD	GEDDDDIKADIT	244	
GEL	-	---GPKPALPA	GTEDTA-KEDAA	293	
VIL	N	HVLGKRRELKA	AVPDTV-VEPAL	249	2
ADS	-	---GGK---KD	YQTS-PLLESQA	609	
GEL	-	---GGK---AA	YRTS-PLKDKK	661	
VIL	-	---GGK---AP	YANT-KRLQEEEN	614	5
ADS	K	DWRDRDQSDGF	GKVVVTEKVAH	367	
GEL	K	NWRDPPDQTDGL	GLSYLSSHIAN	416	
VIL	Q	KWTASNRTSGL	GKTHTVGSVAK	369	3
ADS	G	WDSSRW		715	
GEL	G	WDDDYWSVDPL	-DRAMAELIAA	782	
VIL	A	WDPFKWSNNTKS	YEDLKAESGN	734	6



Fig. 5E

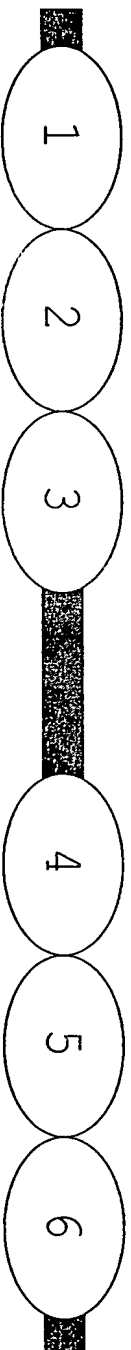
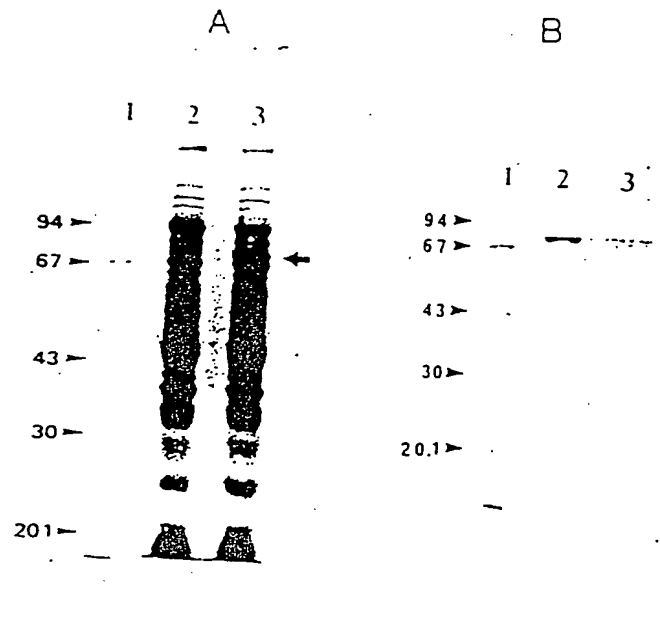


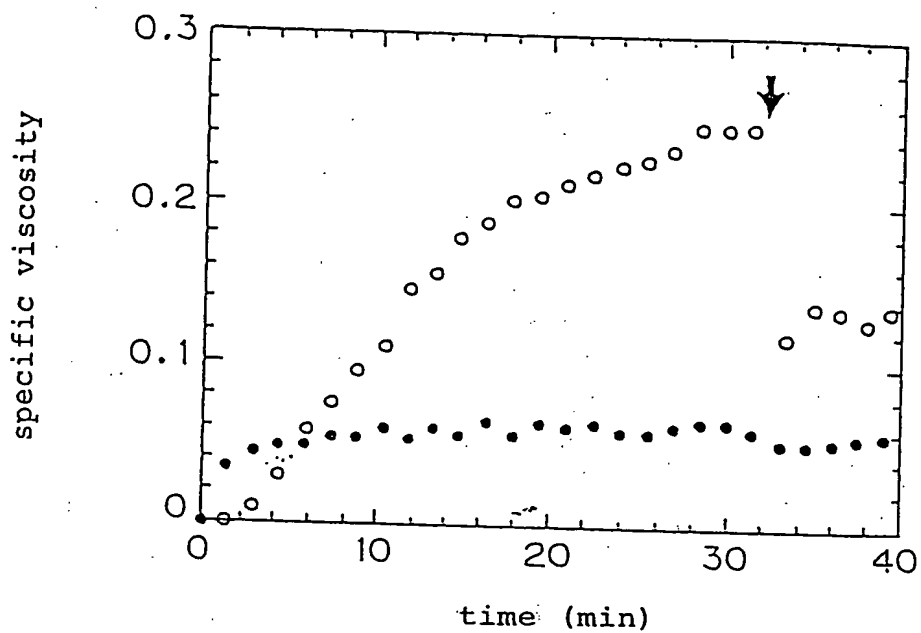
Fig. 6



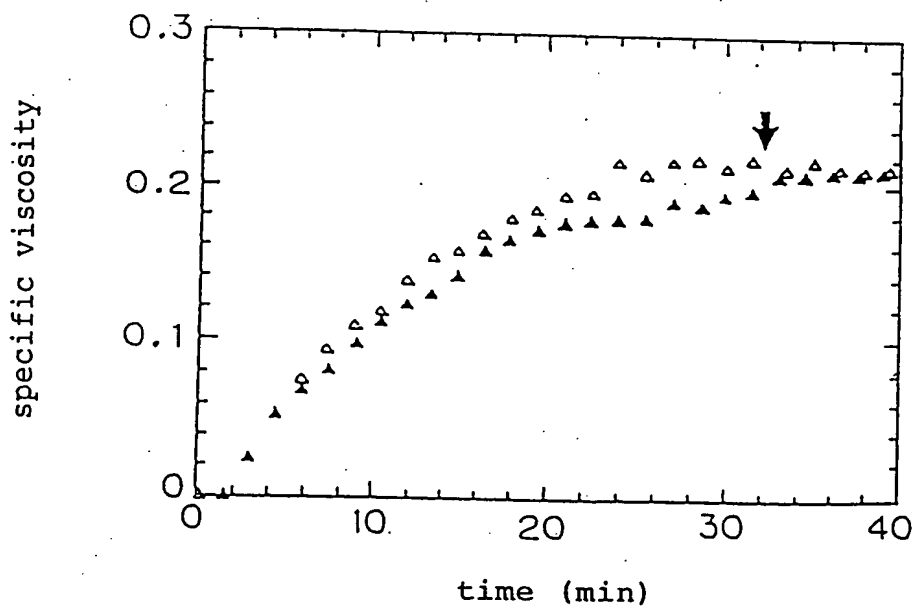
7/9

Fig. 7

A



B



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Fig. 8

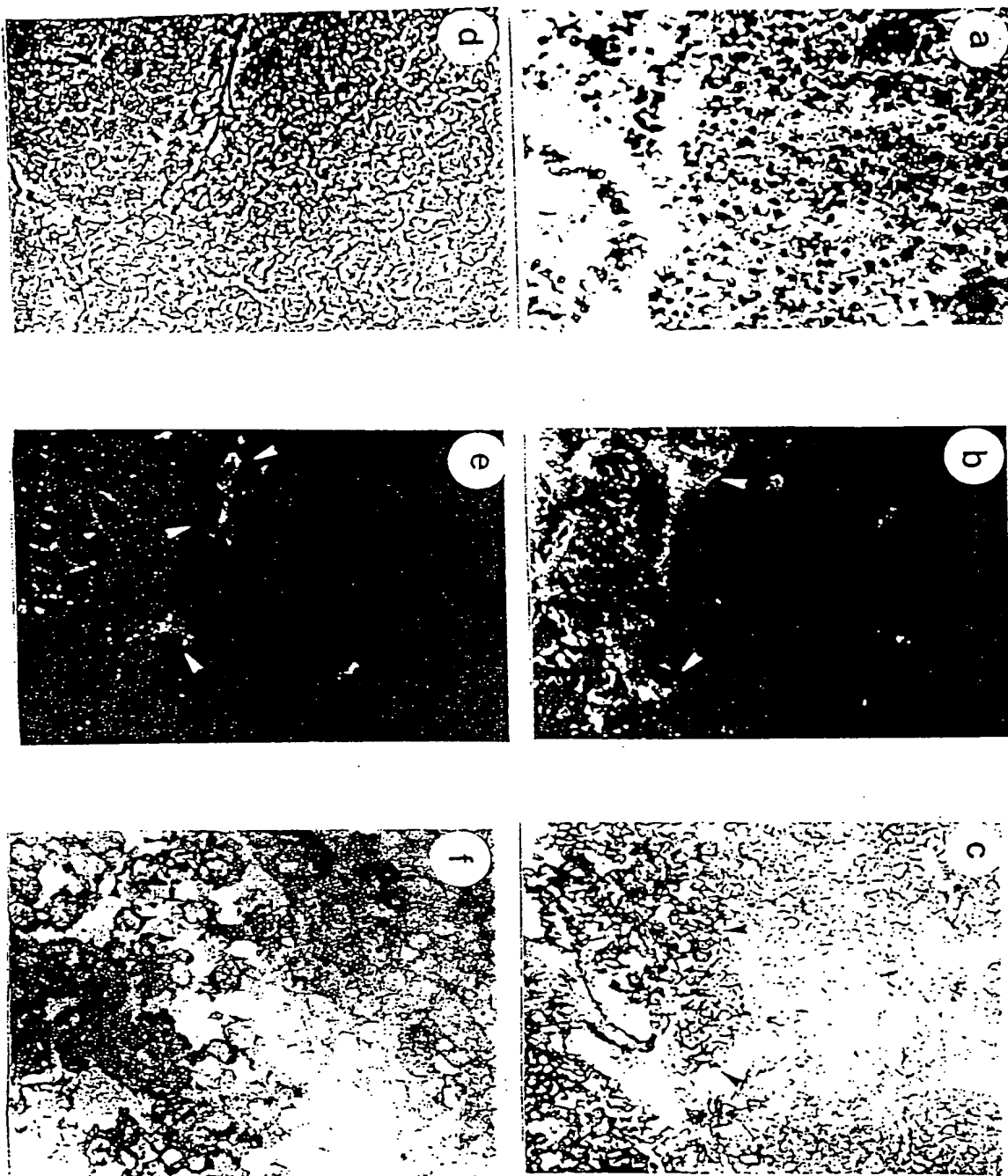


Fig. 9

1' MARELYHEEFARAGKQAGLQVHRIEKLELYPVPSAHGDFYVGDAYLVLHTAKTSRGFTY

 1" MAQGLYHEEFARAGKRAGLQVHRIEKLELYVPESAYGNFYVGDAYLVLHTTQASRGFTY

 61' HLHFWLGKECSQDESTAAAIFTVQMDOYLGGKPVQNRRELQGYESNDFVSYFKGGLKYKAG

 61" RLHFWLGKECTQDESTAAAIFTVQMDOYLGGKPVQNRRELQGYESTDFVGYFKGGLKYKAG

 121' GVASGLNHVLTNDLTAKRLHVKGRVVRATEVPLSWDSFNKGDCFIIDLGTETIYQWCGS

 121" GVASGLNHVLTNDLTACRLHVKGRVVRATEVPLSWDSFNKGDCFIIDLGTETIYQWCGS

 181' SCNKYERLKANQVATGIRYNERKGRSELIWEEGSEPSSELIKVLGEKPELPOGGD000II

 181" SCNKYERLKASQVAIGIRONERKGRAQLIWEEGSEPSSELTKVLGEKPKLRDGED000IK

 241' ADISNRKMAKLYMVSDASGSMRVTVVAEENPFMSMAMLLSEECFILDHGAAKQIFVWKGD

 241" ADITNRKMAKLYMVSDASGSMKVSVAEENPFMSMAMLLSEECFILDHGAAKQIFVWKGD

 301' ANPQERKAAMKTAEFLOQMNYSKNTQIQVLPEGGETPIFKQFFKDWRDKDQSDGFGKVY

 301" ANPQERKAAMKTAEFLOQMNYSTNTQIQVLPEGGETPIFKQFFKDWRDRDQSDGFGKVY

 361' VTEKVAQIKQIPFDASKLHSSPQMAAQHNMVDDGSGKVEIWRVENNGRIQVDQNSYGEFY

 361" VTEKVAHVQKIPFDASKLHSSPQMAAQHHVDDGSGKVQIWRVENNGRVEIDRNSYGEFY

 421' GGDCYIILYTYPRGQIIYTWQGANATRDLTTSFALTQVQLDRSLGGQAVQIRVSQGKEPV

 421" GGDCYIILYTYPRGQIIYTWQGANATRDLTTSFALTQVQLDRSLGGQAVQIRVSQGKEPA

 481' HLLSLFKDKPLIIYKNGTSKKGGQAPAPPTRLFQVRRNLASITRIVEVDVDANSLNSNOV

 481" HLLSLFKDKPLIIYKNGTSKKEGQAPAPPIRLFQVRRNLASITRIMEVDVDANSLNSNOV

 541' CVLKL PQNSGYI WVGKGASQEEKGA EYVASVLKCKTLRIQEGEPEEFWNSLGGKKDYQ

 541" FVLKL RQNGYI WIGKGSTQEEKGA EYVASVLKCKTSTIQEGKEPEEFWNSLGGKKDYQ

 601' TSPLLETQAEDHPPRLYGCSNKTGRFVIEEIPGEFTQOOLAEDOVMLLOAWEQIFIWIGK

 601" TSPLLESQAEDHPPRLYGCSNKTGRFIEEVPGEFTQOOLAEDOVMLLOAWEQIFIWIGK

 661' DANEVEKKESLKSAMYLETOPSGROKRTPIVIIKQGHEPPTFTGWFLGNOSKRW

 661" DANEVEKSESLSAKIYLETOPSGROKRTPIVIIKQGHEPPTFTGWFLGNOSRW